

RAW SEQUENCE LISTING

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Application Serial Number: 10/588,323
Source: JFWP
Date Processed by STIC: 08/11/2006

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/588,323

DATE: 08/11/2006
TIME: 11:03:16

Input Set : A:\253780.txt
Output Set: N:\CRF4\08112006\J588323.raw

3 <110> APPLICANT: Astellas US LLC
4 MAGILAVY, Daniel
6 <120> TITLE OF INVENTION: METHODS OF TREATING SKIN DISORDERS
8 <130> FILE REFERENCE: 253780
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/588,323
C--> 10 <141> CURRENT FILING DATE: 2006-08-03
10 <150> PRIOR APPLICATION NUMBER: 60/542,311
11 <151> PRIOR FILING DATE: 2004-02-06
13 <150> PRIOR APPLICATION NUMBER: PCT/US2005/003907
14 <151> PRIOR FILING DATE: 2005-02-07
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 753
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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27 <221> NAME/KEY: CDS
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32 <222> LOCATION: (1)..(84)
34 <220> FEATURE:
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36 <222> LOCATION: (1)..(750)
37 <223> OTHER INFORMATION: "Human transmembrane LFA-3"
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40 <221> NAME/KEY: mat_peptide
41 <222> LOCATION: (85)..(750)
43 <220> FEATURE:
44 <221> NAME/KEY: misc_feature
45 <222> LOCATION: (646)..(646)
46 <223> OTHER INFORMATION: "Transmembrane domain"
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53 gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt tcc caa caa
54 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
55 -10 -5 -1 1
57 ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta cca agc aat
58 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
59 5 10 15 20

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61	gtg	cct	tta	aaa	gag	gtc	cta	tgg	aaa	aaa	caa	aag	gat	aaa	gtt	gca	192	
62	Val	Pro	Leu	Lys	Glu	Val	Leu	Trp	Lys	Lys	Gln	Lys	Asp	Lys	Val	Ala		
63				25					30						35			
65	gaa	ctg	gaa	aat	tct	gaa	ttc	aga	gct	ttc	tca	tct	ttt	aaa	aat	agg	240	
66	Glu	Leu	Glu	Asn	Ser	Glu	Phe	Arg	Ala	Phe	Ser	Ser	Phe	Lys	Asn	Arg		
67				40					45						50			
69	gtt	tat	tta	gac	act	gtg	tca	ggt	agc	ctc	act	atc	tac	aac	tta	aca	288	
70	Val	Tyr	Leu	Asp	Thr	Val	Ser	Gly	Ser	Leu	Thr	Ile	Tyr	Asn	Leu	Thr		
71				55					60						65			
73	tca	tca	gat	gaa	gat	gag	tat	gaa	atg	gaa	tcg	cca	aat	att	act	gat	336	
74	Ser	Ser	Asp	Glu	Asp	Glu	Tyr	Glu	Met	Glu	Ser	Pro	Asn	Ile	Thr	Asp		
75				70					75						80			
77	acc	atg	aag	ttc	ttt	ctt	tat	gtg	ctt	gag	tct	cca	tct	ccc	aca	384		
78	Thr	Met	Lys	Phe	Phe	Leu	Tyr	Val	Leu	Glu	Ser	Leu	Pro	Ser	Pro	Thr		
79	85				90					95					100			
81	cta	act	tgt	gca	ttg	act	aat	gga	agc	att	gaa	gtc	caa	tgc	atg	ata	432	
82	Leu	Thr	Cys	Ala	Leu	Thr	Asn	Gly	Ser	Ile	Glu	Val	Gln	Cys	Met	Ile		
83				105					110						115			
85	cca	gag	cat	aac	agc	cat	cga	gga	ctt	ata	atg	tac	tca	tgg	gat	480		
86	Pro	Glu	His	Tyr	Asn	Ser	His	Arg	Gly	Leu	Ile	Met	Tyr	Ser	Trp	Asp		
87				120					125						130			
89	tgt	cct	atg	gag	caa	tgt	aaa	cgt	aac	tca	acc	agt	ata	tat	ttt	aag	528	
90	Cys	Pro	Met	Glu	Gln	Cys	Lys	Arg	Asn	Ser	Thr	Ser	Ile	Tyr	Phe	Lys		
91				135					140						145			
93	atg	gaa	aat	gat	ctt	cca	caa	aaa	ata	cag	tgt	act	ctt	agc	aat	cca	576	
94	Met	Glu	Asn	Asp	Leu	Pro	Gln	Lys	Ile	Gln	Cys	Thr	Leu	Ser	Asn	Pro		
95				150					155						160			
97	tta	ttt	aat	aca	aca	tca	tca	atc	att	ttg	aca	acc	tgt	atc	cca	agc	624	
98	Leu	Phe	Asn	Thr	Thr	Ser	Ser	Ile	Ile	Ile	Leu	Thr	Thr	Cys	Ile	Pro	Ser	
99	165				170					175					180			
101	agc	ggt	cat	tca	aga	cac	aga	tat	gca	ctt	ata	ccc	ata	cca	tta	gca	672	
102	Ser	Gly	His	Ser	Arg	His	Arg	Tyr	Ala	Leu	Ile	Pro	Ile	Pro	Leu	Ala		
103					185					190					195			
105	gta	att	aca	aca	tgt	att	gtg	ctg	tat	atg	aat	ggt	att	ctg	aaa	tgt	720	
106	Val	Ile	Thr	Thr	Cys	Ile	Val	Leu	Tyr	Met	Asn	Gly	Ile	Leu	Lys	Cys		
107					200					205					210			
109	gac	aga	aaa	cca	gac	aga	acc	aac	tcc	aat	tga					753		
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125	Val	Cys	Leu	Leu	His	Cys	Phe	Gly	Phe	Ile	Ser	Cys	Phe	Ser	Gln	Gln		
126					-10				-5						-1	1		
129	Ile	Tyr	Gly	Val	Val	Tyr	Gly	Asn	Val	Thr	Phe	His	Val	Pro	Ser	Asn		

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130 5          10          15          20
133 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
134          25          30          35
137 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
138          40          45          50
141 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
142          55          60          65
145 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
146          70          75          80
149 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
150 85          90          95          100
153 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
154          105         110         115
157 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
158          120         125         130
161 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
162          135         140         145
165 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
166          150         155         160
169 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
170 165         170         175         180
173 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
174          185         190         195
177 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
178          200         205         210
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182          215         220
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193 <222> LOCATION: (1)..(720)
195 <220> FEATURE:
196 <221> NAME/KEY: sig_peptide
197 <222> LOCATION: (1)..(84)
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (1)..(720)
202 <223> OTHER INFORMATION: "Human PI-linked LFA-3"
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205 <221> NAME/KEY: mat_peptide
206 <222> LOCATION: (85)..(720)
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211 <223> OTHER INFORMATION: "signal sequence for PI-linkage"
213 <400> SEQUENCE: 3

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Input Set : A:\253780.txt
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214 atg gtt gct ggg agc gac gcg ggg cg	ctg ggg gtc ctc agc gtg	48
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218 gtc tgc ctg ctg cac tgc ttt ggt ttc	atc agc tgt ttt tcc caa caa	96
219 Val Cys Leu Leu His Cys Phe Gly Phe	Ile Ser Cys Phe Ser Gln Gln	
220 -10	-5	-1 1
222 ata tat ggt gtt gtg tat ggg aat gta	act ttc cat gta cca agc aat	144
223 Ile Tyr Gly Val Val Tyr Gly Asn Val	Thr Phe His Val Pro Ser Asn	
224 5 10	15	20
226 gtg cct tta aaa gag gtc cta tgg aaa	aaa caa aag gat aaa gtt gca	192
227 Val Pro Leu Lys Glu Val Leu Trp Lys	Lys Gln Lys Asp Lys Val Ala	
228 25	30	35
230 gaa ctg gaa aat tct gaa ttc aga gct	ttc tca tct ttt aaa aat agg	240
231 Glu Leu Glu Asn Ser Glu Phe Arg Ala	Phe Ser Ser Phe Lys Asn Arg	
232 40	45	50
234 gtt tat tta gac act gtg tca ggt agc	ctc act atc tac aac tta aca	288
235 Val Tyr Leu Asp Thr Val Ser Gly Ser	Leu Thr Ile Tyr Asn Leu Thr	
236 55	60	65
238 tca tca gat gaa gat gag tat gaa atg	gaa tcg cca aat att act gat	336
239 Ser Ser Asp Glu Asp Glu Tyr Glu Met	Glu Ser Pro Asn Ile Thr Asp	
240 70	75	80
242 acc atg aag ttc ttt ctt tat gtg ctt	gag tct ctt cca tct ccc aca	384
243 Thr Met Lys Phe Leu Tyr Val Leu Glu	Ser Leu Pro Ser Pro Thr	
244 85 90	95	100
246 cta act tgt gca ttg act aat gga agc	att gaa gtc caa tgc atg ata	432
247 Leu Thr Cys Ala Leu Thr Asn Gly Ser	Ile Glu Val Gln Cys Met Ile	
248 105	110	115
250 cca gag cat tac aac agc cat cga gga	ctt ata atg tac tca tgg gat	480
251 Pro Glu His Tyr Asn Ser His Arg Gly	Leu Ile Met Tyr Ser Trp Asp	
252 120	125	130
254 tgt cct atg gag caa tgt aaa cgt aac	tca acc agt ata tat ttt aag	528
255 Cys Pro Met Glu Gln Cys Lys Arg Asn	Ser Thr Ser Ile Tyr Phe Lys	
256 135	140	145
258 atg gaa aat gat ctt cca caa aaa ata	cag tgt act ctt agc aat cca	576
259 Met Glu Asn Asp Leu Pro Gln Lys Ile	Gln Cys Thr Leu Ser Asn Pro	
260 150	155	160
262 tta ttt aat aca aca tca tca atc att	ttg aca acc tgt atc cca agc	624
263 Leu Phe Asn Thr Thr Ser Ser Ile Ile	Leu Thr Thr Cys Ile Pro Ser	
264 165 170	175	180
266 agc ggt cat tca aga cac aga tat gca	ctt ata ccc ata cca tta gca	672
267 Ser Gly His Ser Arg His Arg Tyr Ala	Leu Ile Pro Ile Pro Leu Ala	
268 185	190	195
270 gta att aca aca tgt att gtg ctg tat	atg aat ggt atg tat gct ttt	720
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277 <210> SEQ ID NO: 4		
278 <211> LENGTH: 240		
279 <212> TYPE: PRT		

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DATE: 08/11/2006
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Input Set : A:\253780.txt
Output Set: N:\CRF4\08112006\J588323.raw

280 <213> ORGANISM: Homo sapiens
 282 <400> SEQUENCE: 4
 284 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
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 288 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
 289 -10 -5 -1 1
 292 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 293 5 10 15 20
 296 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 297 25 30 35
 300 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 301 40 45 50
 304 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 305 55 60 65
 308 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 309 70 75 80
 312 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 313 85 90 95 100
 316 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 317 105 110 115
 320 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 321 120 125 130
 324 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
 325 135 140 145
 328 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 329 150 155 160
 332 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 333 165 170 175 180
 336 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 337 185 190 195
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 361 <223> OTHER INFORMATION: "Human CD2"
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 364 <221> NAME/KEY: mat_peptide
 365 <222> LOCATION: (73)..(1053)

VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date